



Attachment #4

SEQUENCE LISTING

<110> BROUN, Pierre  
VAN DE LOO, Frank  
BODDUPALLI, Sekhar  
SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY  
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921  
<141> 1999-03-04

<150> 08/597,313  
<151> 1996-02-06

<150> PCT/US97/02187  
<151> 1997-02-06

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attctggtgt taacagtgtca gtttatccctc gggtggccctt tttatcttagc cttaatgtta 180  
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ttacctcaact atgattcaac cgagtggaa tggatttagag gagctttgtt tacggtagac 480  
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atcatatgtt taactgttca ttgcgttcc gatggccctt tttacttagc cttcaacgtt 180  
tctggcagac cttacaatgg ttgcgttcc catttcttcc ccaatgttcc tatctacaac 240  
gaccgtgaac gtcctccagat ttacatctct gatgctggta ttcttagccgt ctgttatgg 300  
ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg 360  
cttctgatag ttaactttttt cttcgcttgc atcacttact tacaacacac tcaccctgcg 420

ttgccttact atgattcatc agagtgggat tggcttagag gagcttttagc tactgttagac 480  
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<223> any

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Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
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Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser
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Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
65							70							75	80
Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys
	85							90						95	
Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	Glu	Cys	Gly	His	His	Ala
	100							105						110	
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His
	115						120							125	
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
	130						135							140	
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro
	145						150							155	160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro
	165							170						175	
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	Phe	Ile	Leu	Gly	Trp	Pro
	180							185						190	
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
	195							200						205	
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu
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Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
	225							230						235	240
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr
	245							250						255	
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	260								265					270	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp
	275							280						285	
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290							295						300	
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
	305							310						315	320
Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Glu	Ala
	325							330						335	
Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	Phe	Asp	Gly	Thr	Pro	Trp
	340							345						350	

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 Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu  
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 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys  
 35 40 45  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110  
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125  
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140  
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser  
 165 170 175  
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190  
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205  
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220  
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp  
 290 295 300  
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val  
 305 310 315 320  
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
 355 360 365  
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 370 375 380  
 Asn Lys Tyr  
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 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
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 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
 195 200 205  
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
 225 230 235 240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr  
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 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
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 <212> PRT  
 <213> Brassica napus

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 35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser  
 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe  
 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
 145 150 155 160

Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly  
 165 170 175

Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr  
 180 185 190

Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys  
 195 200 205

His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220

Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu  
 225 230 235 240

Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg  
 245 250 255

Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300

Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu  
 305 310 315 320

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335

Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val  
 340 345 350

Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
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Phe	Ser	Leu	Ile	Ala	Trp	Pro	Ile	Tyr	Trp	Val	Leu	Gln	Gly	Cys	Leu
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Leu	Thr	Arg	Val	Cys	Gly	His	His	Ala	Phe	Ser	Lys	Tyr	Gln	Trp	Val
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Asp	Asp	Val	Val	Gly	Leu	Thr	Leu	His	Ser	Thr	Leu	Leu	Val	Pro	Tyr
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Phe	Ser	Trp	Lys	Ile	Ser	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser
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Leu	Asp	Arg	Asp	Glu	Arg	Val	Lys	Val	Ala	Trp	Phe	Ser	Lys	Tyr	Leu
100							105					110			
Asn	Asn	Pro	Leu	Gly	Arg	Ala	Val	Ser	Leu	Leu	Val	Thr	Leu	Thr	Ile
115							120					125			
Gly	Trp	Pro	Met	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp
130							135				140				
Ser	Phe	Ala	Ser	His	Tyr	His	Pro	Tyr	Arg	Val	Arg	Leu	Leu	Ile	Tyr
145							150				155			160	
Val	Ser	Asp	Val	Ala	Leu	Phe	Ser	Val	Thr	Tyr	Ser	Leu	Tyr	Arg	Val
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Ala	Thr	Leu	Lys	Gly	Leu	Val	Trp	Leu	Leu	Cys	Val	Tyr	Gly	Val	Pro
180							185					190			
Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Thr	Ile	Thr	Tyr	Leu	Arg	Val
195							200					205			
His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu	Lys	Gly	Ala	Leu	Ala	Thr
210							215				220				
Met	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	His	Ile	Thr
225							230				235			240	
Asp	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His
245							250					255			
Leu	Arg	Val	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Asp	Thr
260							265					270			

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val  
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Lys Tyr Leu Arg Val  
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Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val  
35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly  
50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu  
85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg  
100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu  
115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala  
165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe  
180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp  
195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr  
245 250 255

Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala  
260 265 270

Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly  
275 280 285

Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val  
290 295 300

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<211> 371

<212> PRT

<213> Zea mays

<400> 10

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20 25 30

Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro  
35 40 45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His  
50 55 60

Asp Leu Val Ile Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile  
65 70 75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp  
85 90 95

Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val  
100 105 110

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys  
115 120 125

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp  
130 135 140

Glu Val Phe Val Pro Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro  
145 150 155 160

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln  
165 170 175

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg  
180 185 190

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr  
195 200 205

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val  
210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
 225 230 235 240  
 Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp  
 245 250 255  
 Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His  
 260 265 270  
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met  
 275 280 285  
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp  
 290 295 300  
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala  
 305 310 315 320  
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His  
 325 330 335  
 Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu  
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 Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn  
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 Lys Lys Phe  
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 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr  
 35 40 45  
 Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser  
 50 55 60  
 Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 65 70 75 80  
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe  
 85 90 95  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro  
 100 105 110  
 Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser  
 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile  
130 135 140

Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu  
145 150 155 160

Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His  
165 170 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly  
180 185 190

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe  
195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro  
210 215 220

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<210> 13  
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<220>  
<223> Description of Artificial Sequence: homologous  
regions of Ricinus communis deduced by hydroxylase  
sequence and Arabidopsis thaliana deduced desaturase  
sequence for use as oligonucleotide primer

<400> 13  
cggttaccaga aaacgccttg 20

<210> 14  
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<220>  
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regions of Ricinus communis deduced by hydroxylase  
sequence and Arabidopsis thaliana deduced  
desaturase sequence for use as oligonucleotide primer

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<222> 6, 12, 15  
<223> any

<400> 14  
taywsncaym gnmgnccayca 20

<210> 15  
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regions of *Ricinus communis* deduced by hydroxylase  
sequence and *Arabidopsis thaliana* deduced  
desaturase sequence for use as oligonucleotide primer

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<222> 7, 10, 16  
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21